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LOCUS HMEK1 NUC 3911 BP DS-

1	CGGCCTGGAA	GCACGAGTGG	TTGGAAAGGA	GAAATAGGCG	AGGGCCTGTG	GTGGTAAAAAC
61	CAATCCCAGT	TAAAGGAGAT	GGATCTGAAA	TGAATCACTT	AGCAGCTGAG	TCTCCAGGAG
121	AGGTCCAGGC	AAGTGC GGCT	TCACCAGCTT	CCAAAGGCCG	ACGCAGTCCT	TCTCCTGGCA
181	ACTCCCCATC	AGGTGCGACA	GTGAAATCAG	AATCTCCAGG	AGTAAGGAGA	AAAAGAGTTT
241	CCCCAGTGCC	TTTTCAGAGT	GGCAGAATCA	CACCACCCCG	AAGAGCCCCT	TCACCAGATG
301	GCTTCTCACC	ATATAGCCCT	GAGGAAACAA	ACCGCCGTGT	TAACAAAGTG	ATGCGGGCCA
361	GACTGTACTT	ACTGCGCAG	ATAGGGCCTA	ACTCTTTCCT	GATTGGAGGA	GACAGCCCAG
421	ACAATAAATA	CCGGGTGTTT	ATTGGGCCTC	AGAACTGCAG	CTGTGCACGT	GGAACATTCT
481	GTATTCATCT	GCTATTTGTG	ATGCTCCGGG	TGTTTCAACT	AGAACCCTCA	GACCCAATGT
541	TATGGAGAAA	AACTTTAAAG	AAATTTTGAGG	TTGAGAGTTT	GTTCCAGAAA	TATCACAGTA
601	GGCGTAGCTC	AAGGATCAAA	GCTCCATCTC	GTAACACCAT	CCAGAAGTTT	GTTTCACGCA
661	TGTCAAATTC	TCATACATG	TCATCATCTA	GTAACACCAT	ATCTAGTTCA	GTAACACGCA
721	TAAAGGATGA	AGAGGAACAG	ATGTGTCCTA	TTTGCTTGTT	GGGCATGCTT	GATGAAGAAA
781	GTCTTACAGT	GTGTGAAGAC	GGCTGCAGGA	ACAAGCTGCA	CCACCACTGC	ATGTCAATTT
841	GGGCAGAGA	GTGTAGAAGA	AATAGAGAAC	CTTTAATATG	TCCCCCTTGT	AGATCTAAGT
901	GGAGATCTCA	TGATTTCTAC	AGCCACGAGT	TGTCAAGTCC	TGTGGATTCC	CCTTCTTCCC
961	TCAGAGCTGC	ACAGCAGCAA	ACCGTACAGC	AGCAGCCTTT	GGCTGGATCA	CGAAGGAATC
1021	AAGAGAGCAA	TTTTAACCTT	ACTCATTATG	GAACCTCAGC	AATCCCTCCT	GCTTACAAAG
1081	ATTTAGCTGA	GCCATGGATT	CAGGTGTTTG	GAATGGAACT	CGTTGGCTGC	TTATTCTCTA
1141	GAAACTGGAA	CGTAAGGGAA	ATGGCCCTTA	GGCGTCTTTC	CCACGACGTT	AGTGGGGCCC
1201	TGTTGTTGGC	AAACGGGGAG	AGCACTGGAA	ACTCTGGAGG	CGGCAGTGGG	GGCAGCTTAA
1261	GCGCGGGAGC	GGCCAGCGGG	TCCTCCCAGC	CCAGCATCTC	AGGGGATGTG	GTGGAGGCGT
1321	GCTGCACTGT	CCTGTCTATA	GTCTGCGCTG	ACCCTGTCTA	CAAAGTGTAC	GTTGCTGCTT
1381	TAAAAACATT	GAGAGCCATG	CTGGTATACA	CTCCTTGCCA	CAGTCTGGCA	GAAAGAATCA
1441	AACTTCAGAG	ACTCCTCCGG	CCAGTTGTAG	ACACTATCCT	TGTCAAGTGT	GCAGATGCCA
1501	ACAGCCGCAC	GAGTCAGCTG	TCCATATCTA	CAGTGTCTGA	ACTCTGCAAT	GGCCAAGCAG
1561	GAAAGCTGGC	GGTTGGGAGA	GAAATACTTA	AAGCTGGGTC	CATCGGGGTT	GGTGGTGTCT
1621	ATTACGTCTT	AAGTTGTATC	CTTGGAACCC	AAGCTGAATC	AAACAACCTG	CAAGAACCTG
1681	TGGGTGCGCT	CTGTCTTATA	GACAGGTTGC	TGTTGGAAAT	TCCTGCTGAA	TTCTATCCTC
1741	ATATTGTCTG	TACTGATGTC	TCACAAGCTG	AGCCTGTTGA	AATCAGGTAC	AAGAAGCTGC
1801	TCTCCCTCTT	AACCTTTGCC	TTGCAATCCA	TTGACAATTC	CCACTCGATG	GTTGCAAGC
1861	TCTCTCGGAG	GATATATCTG	AGCTCTGCCA	GGATGGTGAC	CGCAGTGCCC	GCTGTGTTTT
1921	CCAAGCTGGT	AACCATGCTT	AATGCTTCTG	GCTCCACCCA	CTTCACCAGG	ATGCGCCGGC
1981	GTCTGATGGC	TATCGCGGAT	GAGGTAGAAA	TGCGCGAGGT	CATCCAGCTG	GGTGTGGAGG
2041	ACACTGTGGA	TGGGCATCAG	GACAGCTTAC	AGGCGCTGGC	CCCCGCCAGC	TGTCTAGAAA
2101	ACAGCTCCCT	TGAGCACACA	GTCCATAGAG	AGAAAACCTG	AAAAGGACTA	AGTGCTACGA
2161	GACTGAGTGC	CAGCTCGGAG	GACATTTCTG	ACAGACTGGC	CGGCGTCTCT	GTAGGACTTC
2221	CCAGCTCAAC	AACAACAGAA	CAACCAAAGC	CAGCGGTTCA	AACAAAAGGC	AGACCCACAC
2281	GTCAGTGTTC	GAACCTCTCC	CCTTTGTCTC	ATGCTCAATT	AATGTTCCCA	GCACCATCAG
2341	CCCCTTGTTT	CTCTGCCCGG	TCTGTCCCAG	ATATTTCTAA	GCACAGACCC	CAGGCATTTC
2401	TTCCCTGCAA	AATACCTTCC	GCATCTCCTC	AGACACAGCG	CAAGTTCTCT	CTACAATTCC
2461	AGAGGAACTG	CTCTGAACAC	CGAGACTCAG	ACCAGCTCTC	CCCAGTCTTC	ACTCAGTCAA
2521	GACCCCCACC	CTCCAGTAAC	ATACACAGGC	CAAAGCCATC	CCGACCCGTT	CCGGGCAGTA
2581	CAAGCAAACCT	AGGGGACGCC	ACAAAAAGTA	GCATGACACT	TGATCTGGGC	AGTGCTTCCA
2641	GGTGTGACGA	CAGCTTTGGC	GGCGGCGGCA	ACAGTGGCAA	CGCCGTCTCA	CCCAGCGACG
2701	AGACAGTGTG	CACGCCGGTG	GAGGACAAGT	GCAGGTTAGA	TGTGAACACC	GAGCTCAACT
2761	CCAGCATCGA	GGACCTTCTT	GAAGCATCCA	TGCCTTCAAG	TGACACGACA	GTCATTCTCA
2821	AGTCCGAAGT	CGCCGTCTCT	TCTCCGGAAA	AGGCCGAAAA	TGACGACACC	TACAAAGACG
2881	ACGTCAATCA	TAATCAAAAG	TGCAAAAGAA	AGATGGAAGC	TGAAGAGGAG	GAGGCTTTAG
2941	CGATCGCCAT	GGCGATGTCA	GCGTCTCAGG	ATGCCCTCCC	CATCGTCCCT	CAGCTGCAGG
3001	TGGAAAAATGG	AGAAGATATT	ATCATCATTC	AGCAGGACAC	ACCAGAAACT	CTTCCAGGAC
3061	ATACCAAAGC	GAAACAGCCT	TACAGAGAAG	ACGCTGAGTG	GCTGAAAGGC	CAGCAGATAG
3121	GCCTCGGAGC	ATTTCTTCTT	TGTATATCAG	CTCAAGATGT	GGGAACTGGA	ACTTTAATGG
3181	CTGTAAACAA	GGTGACTTAT	GTCAGAAACA	CATCTTCTGA	GCAAGAAGAA	GTAGTAGAAG
3241	CACTAAGAGA	AGAGATAAGA	ATGATGAGCC	ATCTGAATCA	TCCAAACATC	ATTAGGATGT
3301	TGGGAGCCAC	GTGTGAGAAG	AGCAATTACA	ATCTCTTCAT	TGAATGGATG	GCAGGGGGAT

FIGURE 1A

000150 52020000

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3361 CGGTGGCTCA TTTGCTGAGT AAATATGGAG CCTTCAAAGA ATCAGTAGTT ATTA ACTACA
3421 CTGAACAGTT ACTCCGTGGC CTTTCGTATC TCCATGAGAA CCAGATCATT CACAGAGATG
3481 TCAAAGGTGC CAATTTGCTC ATTGACAGCA CCGGTCAGAG GCTGAGAATT GCAGACTTTG
3541 GAGCTGCAGC CAGGTTGGCA TCAAAAGGAA CTGGTGCAGG AGAGTTTCAG GGACAATTAC
3601 TGGGGACAAT TGCATTCATG GCGCCTGAGG TCCTAAGAGG TCAGCAGTAT GGTAGGAGCT
3661 GTGATGTATG GAGTGTTGGC TGCGCCATTA TAGAAATGGC TTGTGCAAAA CCACCTTGGA
3721 ATGCAGAAAA AACTCCAAT CATCTCGCCT TGATATTTAA GATTGCTAGC GCAACTACTG
3781 CACCGTCCAT CCCGTCACAC CTGTCCCTG GTTTACGAGA TGTGGCTCTT CGTTGTTTAG
3841 AACTTCAGCC TCAGGACCGG CCTCCGTCAA GAGAGCTGCT GAAACATCCG GTCTTCCGTA
3901 CCACGTGGTA G

FIGURE 1B

000050" 52000000

Mouse MEKK1 cDNA

10 20 30 40
GCC CGC GAG AGA AAA TGG CGG CGG CGG CGC GCG ATC CCG CCT CGT
CGG GCG CTC TCT TTT ACC GCC GCC GCC CGC TAG CGC GGA GCA

50 60 70 80 90
CGT CGG GAT TCC CGG GCG CCG CGG CGG CGA GTC CCG AGG CGG CCG
GCA GCC CTA AGG GCC CGC GGC GCC GCC GCT CAG GGC TCC GCC CGC

100 110 120 130
GCG GCG GCG GAG GAG GAG GAG CTC TCC AGG GAA CCG GCG CGC CGC
CGC CGC CGC CTC CTC CTC CTC GAG AGG TCC CTT CGC CGC GCG GGC

140 150 160 170 180
CAG CGG GCG CGG CGG GGC TGC TGC GGC AGC CTG GCA GCG CGG GCC
GTC GCC CGC GCC GCC CCG ACG ACG CCC TCG GAC CGT CGC GCC CGG

190 200 210 220
GCG AGC GCG CGG ACT GGC GGC GGC GGC AGC TGC GCA AAG TGC GGA
CGC TCG CGC GCC TGA CCG CCG CCG CCG TCG ACG CGT TTC ACG CCT

230 240 250 260 270
GTG TGG AGC TGG ACC AGC TGC CCG AGC AGC CGC TCT TCC TCG CCG
CAC ACC TCG ACC TGG TCG ACG GCC TCG TCG GCG AGA AGG AGC GGC

280 290 300 310
CCG CCT CGC CGC CCT GCC CAT CTA CTT CCC CGT CGC CGG AGC CCG
GGC GGA GCG GCG GGA CCG GTA GAT GAA GGG GCA GCG GCC TCG GGC

320 330 340 350 360
CGG ACG CGG CTG CAG GAG CGA GTC GCT TCC AGC CCG CGG CGG GAC
GCC TGC GCC GAC GTC CTC GCT CAG CGA AGG TCG GGC GCC GCC CTG

370 380 390 400
CGC CAC CCC CGG GAG CGG CGA GTC GCT GCG GCT CCC ACT CTG CCG
GCG GTG GGG GCC CTC GCC GCT CAG CGA CGC CGA GCG TGA GAC GGC

410 420 430 440 450
AGC TGG CGG CCG CGC GGG ACA GCG GCG CCC GGA GCC CCG CGG GGG
TCG ACC GCC GGC GCG CCC TGT CGC CGC GGG CCT CGG GGC GCC CCC

460 470 480 490
CCG AGC CGC CCT CTG CAG CGG CCC CCT CCG GTC GAG AGA TGG AGA
GGC TCG GCG GGA GAC GTC GCC GGG CGA GGC CAG CTC TCT ACC TCT

500 510 520 530 540
.

FIGURE 2A

Mouse MEKK1 cDNA

ATA AAG AAA CCC TCA AAG GAC TGC ACA AGA TGG AGG ATC GCC CGG
TAT TTC TTT GGG AGT TTC CTC ACG TGT TCT ACC TCC TAG CGG GCC

550 560 570 580
AGG AGA GAA TGA TCC GGG AGA AGC TCA AGG CGA CCT GTA TGC CGG
TCC TCT CTT ACT AGG CCC TCT TCG AGT TCC GCT GGA CAT ACG GCC

590 600 610 620 630
CCT GGA AGC ACG AGT GGT TGG AGA GGA GGA ACA GGA GAG GCC CTG
GGA CCT TCG TGC TCA CCA ACC TCT CCT CCT TGT CCT CTC CGG GAC

640 650 660 670
TGG TGG TGA AGC CAA TCC CTA TTA AAG GAG ATG GAT CTG AAG TGA
ACC ACC ACT TCG GTT AAG GAT AAT TTC CTC TAC CTA GAC TTC ACT

680 690 700 710 720
ATA ACT TGG CAG CTG AGC CCC AGG GAG AGG GCC AGG CAG GTT CCG
TAT TGA ACC GTC GAC TCG GGG TCC CTC TCC CGG TCC GTC CAA GGC

730 740 750 760
CTG CAC CAG CCC CCA AGG GCC GAC GAA GCC CAT CTC CTG GCA GCT
GAC GTG GTC GGG GGT TCC CGG CTG CTT CGG GTA GAG GAC CGT CGA

770 780 790 800 810
CTC CGT CAG GGC GCT CGG TGA AGC CGG AAT CCC CAG GAG TAA GAC
GAG GCA GTC CCG CGA GCC ACT TCG GGC TTA GGG GTC CTC ATT CTG

820 830 840 850
GGA AAC GAG TGT CCC CGG TGC CTT TCC AGA GTG GCA GAA TCA CAC
CCT TTG CTC ACA GGG GCC ACG GAA AGG TCT CAC CGT CTT AGT GTG

860 870 880 890 900
CAC CCC GAA GAG CCC CAT CAC CGG ATG GCT TCT CCC CGT ACA GCC
GTG GGG CTT CTC GGG GTA GTG GCC TAC CGA AGA GGG GCA TGT CGG

910 920 930 940
CAG AAG AGA CGA GCC GCC GCG TGA ACA AAG TGA TGA GAG CCA GGC
GTC TCC TCT GCT CGG CGG CGC ACT TGT TTC ACT ACT CTC GGT CCG

950 960 970 980 990
TGT ACC TGC TGC AGC AGA TAG GAC CCA ACT CTT TCC TGA TTG GAG
ACA TGG ACG ACG TCG TCT ATC CCG GGT TGA GAA AGG ACT AAC CTC

1000 1010 1020 1030
GAG ACA GTC CAG ACA ATA AAT ACC GGG TGT TTA TTG GGC CAC AGA
CTC TGT CAG GTC TGT TAT TTA TGG CCC ACA AAT AAC CCG GTG TCT

FIGURE 2B

Mouse MEKK1 cDNA

1040 1050 1060 1070 1080
ACT GCA OCT GTG GGC GTG GAG CAT TCT GTA TTC ACC TCT TGT TTG
TGA CGT CGA CAC CCG CAC CTC GTA AGA CAT AAG TGG AGA ACA AAC

1090 1100 1110 1120
TCA TGC TCC GGG TGT TTC AGC TAG AAC CCT CTG ACC CCA TGT TAT
AGT ACG AGG CCC ACA AAG TCG ATC TTG GGA GAC TGG GGT ACA ATA

1130 1140 1150 1160 1170
GGA GAA AAA CTT TAA AAA ATT TCG AGG TTG AGA GTT TGT TCC AGA
CCT CTT TTT GAA ATT TTT TAA AGC TCC AAC TCT CAA ACA AGG TCT

1180 1190 1200 1210
AAT ACC ACA GTA GGC GTA GCT CGA GAA TCA AAG CTC CAT CCC GGA
TTA TGG TGT CAT CCG CAT CGA GCT CTT AGT TTC GAG GTA GGG CCT

1220 1230 1240 1250 1260
ACA CCA TCC AGA AGT TTG TGT CAC GCA TGT CAA ATT CTC ACA CAC
TGT GGT AGG TCT TCA AAC ACA GTG CGT ACA GTT TAA GAG TGT GTG

1270 1280 1290 1300
TGT CAT CGT CTA GCA CAT CCA CAT CTA GTT CAG AAA ACA GCA TCA
ACA GTA GCA GAT CGT GTA GGT GTA GAT CAA GTC TTT TGT CGT AGT

1310 1320 1330 1340 1350
AGG ATG AAG AGG AGC AGA TOT GTC CCA TCT GCT TGC TGG GCA TGC
TCC TAC TTC TCC TCG TCT ACA CAG GGT AGA CGA ACG ACC CGT ACC

1360 1370 1380 1390
TGG ATG AGG AGA GCC TGA CTG TGT GTG AAG ATG GCT GCA GGA ACA
ACC TAC TCC TCT CCG ACT GAC ACA CAC TTC TAC CGA CGT CCT TGT

1400 1410 1420 1430 1440
AGC TGC ACC ACC ATT GCA TGT CCA TCT GGG CGG AAG AGT GTA GAA
TCG ACC TGG TGG TAA CGT ACA GGT AGA CCC GCC TTC TCA CAT CTT

1450 1460 1470 1480
GAA ATA GAG AGC CTT TAA TAT GTC CCC TTT GTA GAT CTA AGT GGA
CTT TAT CTC TCG GAA ATT ATA CAG GGG AAA CAT CTA GAT TCA CCT

1490 1500 1510 1520 1530
GAT CCC ATG ACT TCT ACA GCC ATG AGT TAT CAA GCC CCG TGG AGT
CTA GGG TAC TGA AGA TGT CGG TAC TCA ATA GTT CCG GGC ACC TCA

1540 1550 1560 1570

FIGURE 2C

Mouse MEKK1 cDNA

CCC CCG CCT CCC TGC GAG CTG TCC AGC AGC CAT CCT CCC CGC AGC
GGG GGC GGA GGG ACG CTC GAC AAG TCG TCG GTA GGA GGG GCG TCG
1580 1590 1600 1610 1620
AGC CCG TGG CCG GAT CAC AGC GGA GGA ATC AGC AGA GCA GTT TTA
TCG GGC ACC GGC CTA GTG TCG CCT CCT TAG TCC TCT CGT CAA AAT
1630 1640 1650 1660
ACC TTA CTC ATT TTG GAA CCC AGC AGA TTC CTT CCG CTT ACA AAG
TGG AAT GAG TAA AAC CTT GGG TCG TCT AAG GAA GGC GAA TGT TTC
1670 1680 1690 1700 1710
ATT TGG CCG AGC CAT GGA TTC AGG TGT TTG GAA TGG AAC TCG TTG
TAA ACC GGC TCG GTA CCT AAG TCC ACA AAC CTT ACC TTG AGC AAC
1720 1730 1740 1750
GCT GCT TAT TCT CTA GAA ACT GGA ACG TAA GGG AAA TGG CCC TTA
CGA CGA ATA AGA GAT CTT TGA CCT TGC ATT CCC TTT ACC GGG AAT
1760 1770 1780 1790 1800
GGC GTC TTT CCC ACG ACG TTA GTG GGG CCC TGT TGT TGG CAA ACG
CCG CAG AAA GGG TGC TGC AAT CAC CCC GGG ACA ACA ACC GTT TGC
1810 1820 1830 1840
GGG AGA GCA CTG GAA ACT CTG GAG GCG GCA GTG GGG GCA GCT TAA
CCC TCT CGT GAC CTT TGA GAC CTC CGC CGT CAC CCC CGT CGA ATT
1850 1860 1870 1880 1890
GCG CGG GAG CGG CCA GCG GGT CCT CCC AGC CCA GCA TCT CAG GGG
CGC GCC CTC GCC GGT CGC CCA GGA GGG TCG GGT CGT AGA GTC CCC
1900 1910 1920 1930
ATG TGG TGG AGG CGT GCT GCA GTG TCC TGT CTA TAG TCT GCG CTG
TAC ACC ACC TCC GCA CGA CGT CAC AGG ACA GAT ATC AGA CGC GAC
1940 1950 1960 1970 1980
ACC CTG TCT ACA AAG TGT ACG TTG CTG CTT TAA AAA CAT TGA GAG
TGG GAC AGA TGT TTC ACA TGC AAC GAC GAA ATT TTT GTA ACT CTC
1990 2000 2010 2020
CCA TGC TGG TAT ACA CTC CTT GCC ACA GTC TGG CAG AAA GAA TCA
GGT ACG ACC ATA TGT GAG GAA CGG TGT CAG ACC GTC TTT CTT AGT
2030 2040 2050 2060 2070
AAC TTC AGA GAC TCC TCC GGC CAG TTG TAG ACA CTA TCC TTG TCA

FIGURE 2D

Mouse MEKK1 cDNA

TTG AAG TCT CTG AGG AGG CCG GTC AAC ATC TGT GAT AGG AAC AGT
2080 2090 2100 2110
ACT GTG CAG ATG CCA ACA GCC GCA CGA GTC AGC TGT CCA TAT CTA
TCA CAC GTC TAC GGT TGT CCG CGT GCT CAG TCG ACA GGT ATA GAT
2120 2130 2140 2150 2160
CAG TGC TGG AAC TCT GCA AGG GCC AAG CAG GAG AGC TGG CCG TTG
GTC ACG ACC TTG AGA CGT TCC CGG TTC GTC CTC TCG ACC GCC AAC
2170 2180 2190 2200
GGA GAG AAA TAC TTA AAG CTG GGT CCA TCG GGG TTG GTG GTG TCG
CCT CTC TTT ATG AAT TTC GAC CCA GGT AGC CCC AAC CAC CAC AGC
2210 2220 2230 2240 2250
ATT ACG TCT TAA GTT GTA TCC TTG GAA ACC AAG CTG AAT CAA ACA
TAA TGC AGA ATT CAA CAT AGG AAC CTT TGG TTC GAC TTA GTT TGT
2260 2270 2280 2290
ACT GGC AAG AAC TGC TGG GTC GCC TCT GTC TTA TAG ACA GGT TGC
TGA CCG TTC TTG ACG ACC CAG CGG AGA CAG AAT ATC TGT CCA ACG
2300 2310 2320 2330 2340
TGT TGG AAT TTC CTG CTG AAT TCT ATC CTC ATA TTG TCA GTA CTG
ACA ACC TTA AAG GAC GAC TTA AGA TAG GAG TAT AAC AGT CAT GAC
2350 2360 2370 2380
ATG TCT CAC AAG CTG AGC CTG TTG AAA TCA GGT ACA AGA AGC TGC
TAC AGA GTG TTC GAC TCG GAC AAC TTT AGT CCA TGT TCT TCG ACG
2390 2400 2410 2420 2430
TCT CCC TCT TAA CCT TTG CCT TGC AAT CCA TTG ACA ATT CCC ACT
AGA GGG AGA ATT GGA AAC GGA ACG TTA GGT AAC TGT TAA GGG TGA
2440 2450 2460 2470
CGA TGG TTG GCA AGC TCT CTC GGA GGA TAT ATC TGA GCT CTG CCA
GCT ACC AAC CGT TCG AGA GAG CCT CCT ATA TAG ACT CGA GAC GGT
2480 2490 2500 2510 2520
GGA TGG TGA CCG CAG TGC CCG CTG TGT TTT CCA AGC TGG TAA CCA
CCT ACC ACT GGC GTC ACG GGC GAC ACA AAA GGT TCG ACC ATT GGT
2530 2540 2550 2560
TGC TTA ATG CTT CTG GCT CCA CCC ACT TCA CCA GGA TGC GCC GGC
ACG AAT TAC GAA GAC CCA GGT GGG TGA AGT GGT CCT ACG CCG CCG

FIGURE 2E

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Mouse MEKK1 cDNA

2570 2580 2590 2600 2610
* * * * *
GTC TGA TGG CTA TCG CGG ATG AGG TAG AAA TTG CCG AGG TCA TCC
CAG ACT ACC GAT AGC GCC TAC TCC ATC TTT AAC GGC TCC AGT AGG

2620 2630 2640 2650
* * * * *
AGC TGG GTG TGG AGG ACA CTG TGG ATG GGC ATC AGG ACA GCT TAC
TCG ACC CAC ACC TCC TGT GAC ACC TAC CCG TAG TCC TGT CGA ATG

2660 2670 2680 2690 2700
* * * * *
AGG CCG TGG CCC CCA CCA GCT GTC TAG AAA ACA GCT CCC TTG AGC
TCC GGC ACC GGG GGT GGT CGA CAG ATC TTT TGT CGA GGG AAC TCG

2710 2720 2730 2740
* * * * *
ACA CAG TCC ATA GAG AGA AAA CTG GAA AAG GAC TAA GTG CTA CGA
TGT GTC AGG TAT CTC TCT TTT GAC CTT TTC CTG ATT CAC GAT GCT

2750 2760 2770 2780 2790
* * * * *
GAC TGA GTG CCA GCT CGG AGG ACA TTT CTG ACA GAC TGG CCG GCG
CTG ACT CAC GGT CGA GCC TCC TGT AAA GAC TGT CTG ACC GGC CGC

2800 2810 2820 2830
* * * * *
TCT CTG TAG GAC TTC CCA GCT CAA CAA CAA CAG AAC AAC CAA AGC
AGA GAC ATC CTG AAG GGT CGA GTT GTT GTT GTC TTG TTG GTT TCG

2840 2850 2860 2870 2880
* * * * *
CAG CGG TTC AAA CAA AAG GCA GAC CCC ACA GTC AGT GTT TGA ACT
GTC GCC AAG TTT GTT TTC CGT CTG GGG TGT CAG TCA CAA ACT TGA

2890 2900 2910 2920
* * * * *
CCT CCC CTT TGT CTC ATG CTC AAT TAA TGT TCC CAG CAC CAT CAG
GGA GGG GAA ACA GAG TAC GAG TTA ATT ACA AGG GTC GTG GTA GTC

2930 2940 2950 2960 2970
* * * * *
CCC CTT GTT CCT CTG CCC CGT CTG TCC CAG ATA TTT CTA AGC ACA
GGG GAA CAA GGA GAC GGG GCA GAC AGG GTC TAT AAA GAT TCG TGT

2980 2990 3000 3010
* * * * *
GAC CCC AGG CAT TTG TTC CCT GCA AAA TAC CTT CCG CAT CTC CTC
CTG GGG TCC GTA AAC AAG GGA CGT TTT ATG GAA GGC GTA CAG GAG

3020 3030 3040 3050 3060
* * * * *
AGA CAC AGC GCA AGT TCT CTC TAC AAT TCC AGA GGA ACT GCT CTG
TCT GTG TCG CGT TCA AGA GAG ATG TTA AAG TCT CCT TGA CGA GAC

3070 3080 3090 3100
* * * * *

FIGURE 2F

Mouse MEKK1 cDNA

AAC ACC GAG ACT CAG ACC AGC TCT CCC CAG TCT TCA CTC AGT CAA
TTG TGG CTC TGA GTC TGG TCG AGA GGG GTC AGA AGT GAG TCA GTT

3110 3120 3130 3140 3150
GAC CCC CAC CCT CCA GTA ACA TAC ACA GGC CAA AGC CAT CCC GAC
CTG GGG GTG GGA GGT CAT TGT ATG TGT CCG GTT TCG GTA GGG CTG

3160 3170 3180 3190
CCG TTC CGG GCA GTA CAA GCA AAC TAG GGG ACG CCA CAA AAA GTA
GGC AAG GCC CGT CAT GTT CGT TTG ATC CCC TGC GGT GTT TTT CAT

3200 3210 3220 3230 3240
GCA TGA CAC TTG ATC TGG GCA GTG CTT CCA GGT GTG ACG ACA GCT
CGT ACT GTG AAC TAG ACC CGT CAC GAA GGT CCA CAC TGC TOT CGA

3250 3260 3270 3280
TTG GCG GCG GCG GCA ACA GTG GCA ACG CCG TCA TAC CCA GCG ACG
AAC CGC CGC CGC CGT TGT CAC CGT TGC GGC AGT ATG GGT CGC TGC

3290 3300 3310 3320 3330
AGA CAG TGT TCA CGC CGG TGG AGG ACA AGT GCA GGT TAG ATG TGA
TCT GTC ACA AGT GCG GCC ACC TCC TGT TCA CGT CCA ATC TAC ACT

3340 3350 3360 3370
ACA CCG AGC TCA ACT CCA GCA TCG AGG ACC TTC TTG AAG CAT CCA
TGT GGC TCG AGT TGA GGT CGT AGC TCC TGG AAG AAC TTC GTA GGT

3380 3390 3400 3410 3420
TGC CTT CAA GTG ACA CGA CAG TCA CTT TCA AGT CCG AAG TCG CCG
ACG GAA GTT CAC TGT GCT GTC AGT GAA AGT TCA GGC TTC AGC GGC

3430 3440 3450 3460
TCC TCT CTC CGG AAA AGG CCG AAA ATG ACG ACA CCT ACA AAG ACG
AGG AGA GAG GCC TTT TCC GGC TTT TAC TGC TGT GGA TGT TTC TGC

3470 3480 3490 3500 3510
ACG TCA ATC ATA ATC AAA AGT GCA AAG AAA AGA TGG AAG CTG AAG
TGC AGT TAG TAT TAG TTT TCA CGT TTC TTT TCT ACC TTC GAC TTC

3520 3530 3540 3550
AGG AGG AAG CTT TAG CGA TCG CCA TGG CGA TGT CAG CGT CTC AGG
TCC TCC TCC GAA ATC GCT AGC GGT ACC GCT ACA GTC GAG TCC

3560 3570 3580 3590 3600
ATG CCC TCC CCA TCG TCC CTC AGC TGC AGG TGG AAA ATG GAG AAG
TAC GGG AGG GGT AGC AGG GAG TCG ACG TCC ACC TTT TAC CTC TTC

FIGURE 2G

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Mouse MEKK1 cDNA

3610 3620 3630 3640
ATA TTA TCA TCA TTC AGC AGG ACA CAC CAG AAA CTC TTC CAG GAC
TAT AAT AGT AGT AAG TCG TCC TGT GTG GTC TTT GAG AAG GTC CTG

3650 3660 3670 3680 3690
ATA CCA AAG CGA AAC AGC CTT ACA GAG AAG ACG CTG AGT GGC TGA
TAT GGT TTC GCT TTG TCG GAA TGT CTC TTC TGC GAC TCA CCG ACT

3700 3710 3720 3730
AAG GCC AGC AGA TAG GCC TCG GAG CAT TTT CTT CCT GTT ACC AAG
TTC CGG TCG TCT ATC CGG AGC CTC GTA AAA GAA GGA CAA TGG TTC

3740 3750 3760 3770 3780
CAC AGG ATG TGG GGA CTG GGA CTT TAA TGG CTG TGA AAC AGG TGA
GTG TCC TAC ACC CCT GAC CCT GAA ATT ACC GAC ACT TTT TCC ACT

3790 3800 3810 3820
CGT ACG TCA GAA ACA CAT CCT CCG AGC AGG AGG AGG TGG TGG AAG
GCA TGC AGT CTT TGT GTA GGA GGC TCG TCC TCC TCC ACC ACC TTC

3830 3840 3850 3860 3870
CGT TGA GGG AAG AGA TCC GGA TGA TGG GTC ACC TCA ACC ATC CAA
GCA ACT CCC TTC TCT AGG CCT ACT ACC CAG TGG AGT TGG TAG GTT

3880 3890 3900 3910
ACA TCA TCC GGA TCC TGG GGG CCA CGT GCG AGA AGA GCA ACT ACA
TGT AGT AGG CCT ACG ACC CCC GGT GCA GCG TCT TCT CGT TGA TGT

3920 3930 3940 3950 3960
ACC TCT TCA TTG AGT GGA TGG CCG GAG GAT CTG TGG CTC ACC TCT
TGG AGA AGT AAC TCA CCT ACC GCC CTC CTA GAC ACC GAG TGG AGA

3970 3980 3990 4000
TGA GTA AAT ACG GAG CTT TCA AGG AGT CAG TCG TCA TTA ACT ACA
ACT CAT TTA TGC CTC GAA AGT TCC TCA GTC AGC AGT AAT TGA TGT

4010 4020 4030 4040 4050
CTG AGC AGT TAC TGC GTG GCC TTT CCT ATC TCC ACG AGA ACC AGA
GAC TCG TCA ATG ACG CAC CGG AAA GGA TAG AGG TGC TCT TGG TCT

4060 4070 4080 4090
TCA TTC ACA GAG ACG TCA AAG GTG CCA ACC TGC TCA TTG ACA GCA
AGT AAG TGT CTC TGC AGT TTC CAC GGT TGG ACG AGT AAC TGT CGT

4100 4110 4120 4130 4140

FIGURE 2H

Mouse MEKK1 cDNA

CCG GTC AGA GGC TGA GAA TTG CAG ACT TTG GAG CTG CTG CCA GGT
GGC CAG TCT CCG ACT CTT AAC GTC TGA AAC CTC GAC GAC GGT CCA

4150 4160 4170 4180
TGG CAT CAA AAG GAA CCG GTG CAG GAG AGT TCC AGG GAC AGT TAC
ACC GTA GTT TTC CTT GGC CAC GTC CTC TCA AGG TCC CTG TCA ATG

4190 4200 4210 4220 4230
TGG GGA CAA TTG CAT TCA TGG CGC CTG AGG TCC TAA GAG GTC AGC
ACC CCT GTT AAC GTA AGT ACC GCG GAC TCC AGG ATT CTC CAG TCG

4240 4250 4260 4270
AGT ATG GTA GGA GCT GTG ATG TAT GGA GTG TTG GCT GCG CCA TTA
TCA TAC CAT CCT CGA CAC TAC ATA CCT CAC AAC CGA CCG GGT AAT

4280 4290 4300 4310 4320
TAG AAA TGG CTT GTG CAA AAC CAC CTT GGA ATG CAG AAA AAC ACT
ATC TTT ACC GAA CAC GTT TTG GTG GAA CCT TAC GTC TTT TTG TGA

4330 4340 4350 4360
CCA ATC ATC TCG CCT TGA TAT TTA AGA TTG CTA GCG CAA CTA CTG
GGT TAG TAG AGC GGA ACT ATA AAT TCT AAC GAT CCG GTT GAT GAC

4370 4380 4390 4400 4410
CAC CGT CCA TCC CGT CAC ACC TGT CCC CCG GTC TCC GCG ACG TGG
GTG GCA GGT AGG GCA GTG TGG ACA GGG GCC CAG ACG CCG TGC ACC

4420 4430 4440 4450
CCG TGC GCT GCT TAG AAC TTC AGC CTC AGG ACC GGC CTC CGT CCA
GGC ACG CGA CGA ATC TTG AAG TCG GAG TCC TGG CCG GAG GCA GGT

4460 4470 4480 4490 4500
GAG AGC TGC TGA AAC ATC CCG TCT TCC GTA CCA CGT GGT AGT TAA
CTC TCG ACG ACT TTG TAG GCC AGA AGG CAT GGT GCA CCA TCA ATT

4510 4520 4530 4540
TTG TTC AGA TCA GCT CTA ATG GAG ACA GGA TAT GCA ACC GGG AGA
AAC AAG TCT AGT CGA GAT TAC CTC TGT CCT ATA CGT TGG CCC TCT

4550 4560 4570 4580 4590
GAG AAA AGA GAA CTT GTG GGC GAC CAT GCU GCT AAC CCG AGC CCT
CTC TTT TCT CTT GAA CAC CCG CTG GTA CCG CGA TTG GCG TCG GGA

4600 4610 4620 4630
CAC GCC ACT GAA CAG CCA GAA ACG GGG CCA GCG GGG AAC CGT ACC

FIGURE 21

Mouse MEKK1 cDNA

GTG CGG TGA CTT GTC GGT CTT TOC CCC GGT CGC CCC TTG GCA TOG
4640 4650 4660 4670 4680
TAA GCA TGT GAT TGA CAA ATC ATG ACC TGT ACC TAA GCT CGA TAT
ATT COT ACA CTA ACT GTT TAG TAC TGG ACA TGG ATT CGA GCT ATA
4690 4700 4710 4720
GCA GAC ATC TAC AGC TCG TOC AGG AAC TGC ACA CCG TGC CTT TCA
CGT CTG TAG ATG TCG AGC ACG TCC TTG ACG TGT GGC ACG GAA AGT
4730 4740 4750 4760 4770
CAG GAC TGG CTC TGG GGG ACC AGG AAG GCG ATG GAG TTT GCA TGA
GTC CTG ACC GAG ACC CCC TGG TCC TTC CGC TAC CTC AAA COT ACT
4780 4790 4800 4810
CTA AAG AAC AGA AGC ATA AAT TTA TTT TTG GAG CAC TTT TTC AGC
GAT TTC TTG TCT TCG TAT TTA AAT AAA AAC CTC GTG AAA AAG TCG
4820 4830 4840 4850 4860
TAA TCA GTA TTA CCA TGT ACA TCA ACA TGC CCG CCA CAT TTC AAA
ATT AGT CAT AAT GGT ACA TGT AGT TGT ACG GGC GGT GTA AAG TTT
4870 4880 4890 4900
CTC AGA CTG TCC CAG ATG TCA AGA TCC ACT GTG TTT GAG TTT GTT
GAG TCT GAC AGG GTC TAC AGT TCT AGG TGA CAC AAA CTC AAA CAA
4910 4920 4930 4940 4950
TGC AGT TCC CTC AGC TTG CTG GTA ATT GTG GTG TTT TGT TTT CGA
ACG TCA AGG GAG TCG AAC GAC CAT TAA CAC CAC AAA ACA AAA GCT
4960 4970 4980 4990
TGC AAA TGT GAT GTA ATA TTC TTA TTT TCT TTG GAT CAA AGC TGG
ACG TTT ACA CTA CAT TAT AAG AAT AAA AQA AAC CTA GTT TCG ACC
5000 5010 5020 5030 5040
ACT GAA AAT TGT ACT GTG TAA TTA TTT TTG TGT TTT TAA TGT TAT
TGA CTT TTA ACA TGA CAC ATT AAT AAA AAC ACA AAA ATT ACA ATA
5050 5060 5070 5080
TTG GTA CTC GAA TTG TAA ATA ACG TCT ACT GCT GTT TAT TCC AGT
AAC CAT GAG CTT AAC ATT TAT TGC AGA TGA CGA CAA ATA AGG TCA
5090 5100 5110 5120 5130
TTC TAC TAC CTC AGG TGT CCT ATA GAT TTT TCT TCT ACC AAA GTT
AAG ATG ATG GAG TCC ACA GGA TAT CTA AAA AQA AGA TGG TTT CAA

FIGURE 2J

Mouse MEKK1 cDNA

5140 5150 5160 5170
CAC TCT CAG AAT GAA ATT CTA CGT GCT GTG TGA CTA TGA CTC CTA
GTG AGA GTC TTA CTT TAA GAT GCA CGA CAC ACT GAT ACT GAG GAT
5180 5190 5200 5210 5220
AGA CTT CCA GGG CTT AAG GGC TAA CTC CTA TTA GCA CCT TAC TAT
TCT GAA GGT CCC GAA TTC CCG ATT GAG GAT AAT CGT GGA ATG ATA
5230 5240 5250
GTA AGC AAA TGC TAC AAA AAA AAA AAA AAA AAA
CAT TCG TTT ACG ATG TTT TTT TTT TTT TTT TTT

FIGURE 2K

[illegible]

hMEKK1/mMEKK1 Protein Alignment

	1	10	20	30	40
mouse	MAAAAGDRAS	SSGFPGAAAA	SPEAGGGGGG	GGALQGSGAP	AAGAAGLLRE
human					
	50	60	70	80	90
mouse	PGSAGRERAD	WRRRQLRKVR	SVELDQLPEQ	PLFLAAASPP	CPSTSPSPEP
human					
	100	110	120	130	140
mouse	ADAAAGASRF	QPAAGPPPPG	AASRCGSHSA	ELAAARDSGA	RSPAGAEPPS
human					
	150	160	170	180	190
mouse	AAAPSGREME	NKETLKGLHK	MEDRPEERMI	REKLKATOMP	AWKHEWLERR
human					AWKHEWLERR
	200	210	220	230	240
mouse	NRRGPVVVKP	IPIKGDGSEV	NNLAAEQGE	GQAGSAAAP	KGRRSPSPGS
human	NRRGPVVVKP	IPVKGDGSEM	NHLAAESPGE	VQASAAASP	KGRRSPSPGN
	250	260	270	280	290
mouse	SPSGRSVKPE	SPGVRRKRVS	FVPFQSGRIT	PPRRAPSPDG	FSPYSPEETS
human	SPSGRIVKSE	SPGVRRKRVS	FVPFQSGRIT	PPRRAPSPDG	FSPYSPEETN
	300	310	320	330	340
mouse	RRVNKVMRAR	LYLLQQIGPN	SFLIGGDSPD	NKYRVFIGPQ	NCSCGRGAF
human	RRVNKVMRAR	LYLLQQIGPN	SFLIGGDSPD	NKYRVFIGPQ	NCSCARGTFC
	350	360	370	380	390
mouse	IHLLEFVMLRV	FQLEPSDPM	WRKTLKNFEV	ESLFQKYHSR	RSSRIKAPSR
human	IHLLEFVMLRV	FQLEPSDPM	WRKTLKNFEV	ESLFQKYHSR	RSSRIKAPSR
	400	410	420	430	440
mouse	NTIQKFVSRM	SNSHILSSSS	TSTSSSENSI	KDEEQMCPI	CLLGMLDEES
human	NTIQKFVSRM	SNSHILSSSS	TSTSSVNSI	KDEEQMCPI	CLLGMLDEES

FIGURE 3A

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hMEKK1/mMEKK1 Protein Alignment

	450	460	470	480	490
mouse	LTVCEDGCRN	KLHHHOMSIW	AEECRNREP	LICPLCRSKW	RS HDFYSHEL
human	LTVCEDGCRN	KLHHHOMSIW	AEECRNREP	LICPLCRSKW	RS HDFYSHEL
	500	510	520	530	540
mouse	SSPVESPA SL	RAVQOPSSPQ	QPVAGSQRRN	QESS FNLTHE	GTQQIPSAVK
human	SSPVDSPS SL	RAAQQQIVQQ	QPLAGS-RRN	QESN FNLTHY	GTQQIPPAYK
	550	560	570	580	590
mouse	DLAEFWIQVF	GMELVGCLFS	RNMNVREMAI	RRLSHDVSGA	LLLANGESTG
human	DLAEFWIQVF	GMELVGCLFS	RNMNVREMAI	RRLSHDVSGA	LLLANGESTG
	600	610	620	630	640
mouse	NSGGGSGGSL	SAGAASGSSQ	PSISGDVEA	CCSVLSIVCA	DPVKVYVAA
human	NSGGGSGGSL	SAGAASGSSQ	PSISGDVEA	CCSVLSIVCA	DPVKVYVAA
	650	660	670	680	690
mouse	LKTLRAMLVY	TPCHSLAERI	KLQRLRPVW	DTILVKCADA	NSRTSQLSIS
human	LKTLRAMLVY	TPCHSLAERI	KLQRLRPVW	DTILVKCADA	NSRTSQLSIS
	700	710	720	730	740
mouse	TVLELCKGQA	GELAVGREIL	KAGSIGVGGV	DYVLSCILGN	QAESNNWQEL
human	TVLELCKGQA	GKLAVGREIL	KAGSIGVGGV	DYVLSCILGN	QAESNNWQEL
	750	760	770	780	790
mouse	LGRICLIDRL	LLEFPAEFYP	HIVSTDVSQA	EPVEIRYKKL	LSLLTFALQS
human	LGRICLIDRL	LLEFPAEFYP	HIVSTDVSQA	EPVEIRYKKL	LSLLTFALQS
	800	810	820	830	840
mouse	IDNSHSMVGK	LSRRIYLSSA	RMVTAVPAVF	SKLVIMLNAS	GSIHFTRMRR
human	IDNSHSMVGK	LSRRIYLSSA	RMVTAVPAVF	SKLVIMLNAS	GSIHFTRMRR
	850	860	870	880	890
mouse	RLMAIADEVE	IAEVIQLGVE	DTVDGHQDSL	QAVAPTSCLE	NSSLEHIVHR
human	RLMAIADEVE	IAEVIQLGVE	DTVDGHQDSL	QALAPASCLE	NSSLEHIVHR

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FIGURE 3B

	900	910	920	930	940
mouse	EKTGKGLSAT	RLSASSEDIS	DRLAGVSVGL	PSSTITTEQPK	PAVQTKGRPH
human	EKTGKGLSAT	RLSASSEDIS	DRLAGVSVGL	PSSTITTEQPK	PAVQTKGRPH
	950	960	970	980	990
mouse	SQCLNSSPLS	HAQLMFPAAPS	APCSSAPSVP	DISKHRPQAF	VPCKIPASAP
human	SQCLNSSPLS	HAQLMFPAAPS	APCSSAPSVP	DISKHRPQAF	VPCKIPASAP
	1000	1010	1020	1030	1040
mouse	QTQRKFSLOF	QRNCSEHRDS	DQLSPVFTQS	RPPPSNNIHR	PKPSRPVFGS
human	QTQRKFSLOF	QRNCSEHRDS	DQLSPVFTQS	RPPPSNNIHR	PKPSRPVFGS
	1050	1060	1070	1080	1090
mouse	TSKLGDAIKS	SMTLDLGSAS	RCDDSFSGGGG	NSGNAVIPSD	ETVFTFVEDK
human	TSKLGDAIKS	SMTLDLGSAS	RCDDSFSGGGG	NSGNAVIPSD	ETVFTFVEDK
	1100	1110	1120	1130	1140
mouse	CRLDVNTELN	SSIEDLLEAS	MPSSDITVIF	KSEVAVLSPE	KAENDDTYKD
human	CRLDVNTELN	SSIEDLLEAS	MPSSDITVIF	KSEVAVLSPE	KAENDDTYKD
	1150	1160	1170	1180	1190
mouse	DVNHNQKCKE	KMEAEEEEFAL	AIAMAMSASQ	DALPIVPQLQ	VENGEDIIII
human	DVNHNQKCKE	KMEAEEEEFAL	AIAMAMSASQ	DALPIVPQLQ	VENGEDIIII
	1200	1210	1220	1230	1240
mouse	QQDTPETLPG	HITAKQPYRE	DAEWLKGQOI	GLGAFSSCYQ	AQDVGIGTLM
human	QQDTPETLPG	HITAKQPYRE	DAEWLKGQOI	GLGAFSSCYQ	AQDVGIGTLM
	1250	1260	1270	1280	1290
mouse	AVKQVTYVRN	TSSEQEEVVE	ALREEIRMMG	HLNHPNIIRM	LGATCEKSNY
human	AVKQVTYVRN	TSSEQEEVVE	ALREEIRMMG	HLNHPNIIRM	LGATCEKSNY
	1300	1310	1320	1330	1340
mouse	NLFIEWMAGG	SVAHLLSKYG	AFKESVVINY	TEQLLRGLSY	LHENQIIHRD
human	NLFIEWMAGG	SVAHLLSKYG	AFKESVVINY	TEQLLRGLSY	LHENQIIHRD

FIGURE 3C

hMEKK1/mMEKK1 Protein Alignment

[illegible]

FIGURE 3D

FIG.4

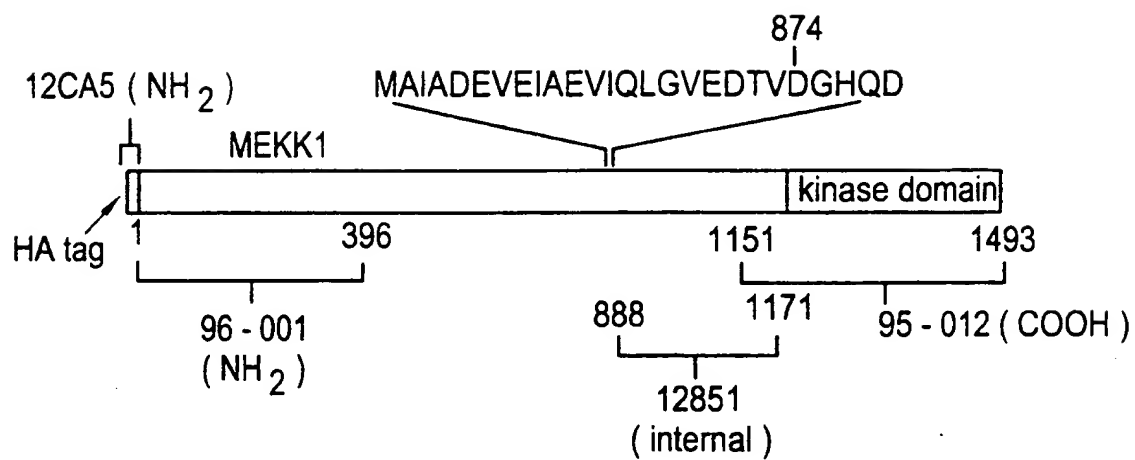


FIG.5

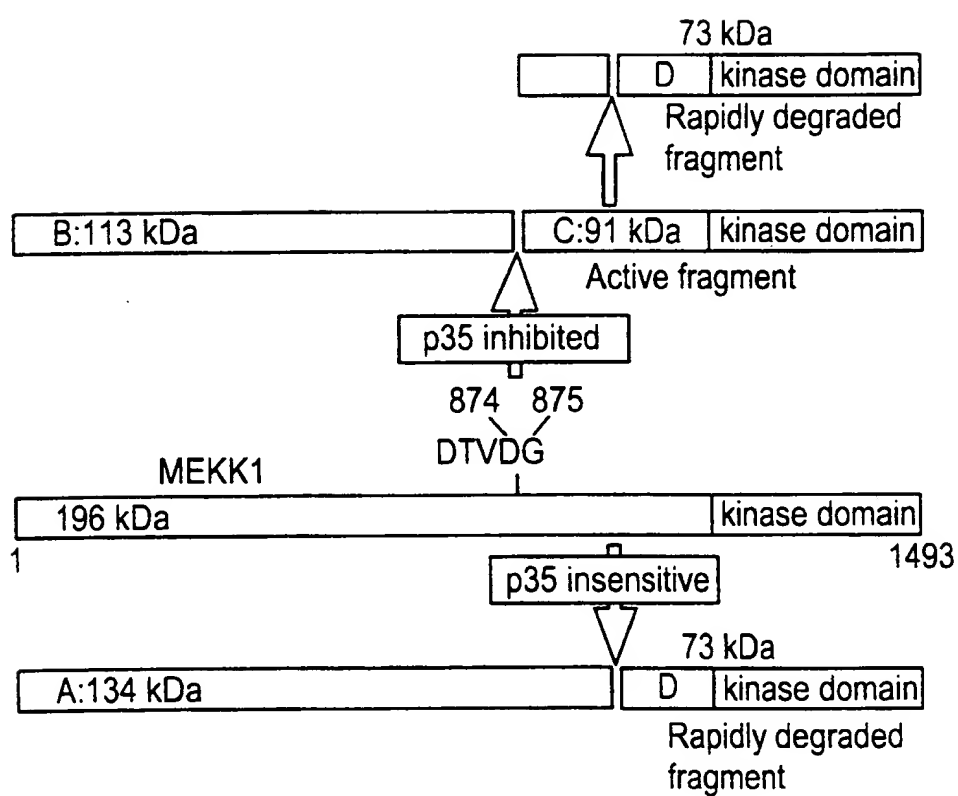
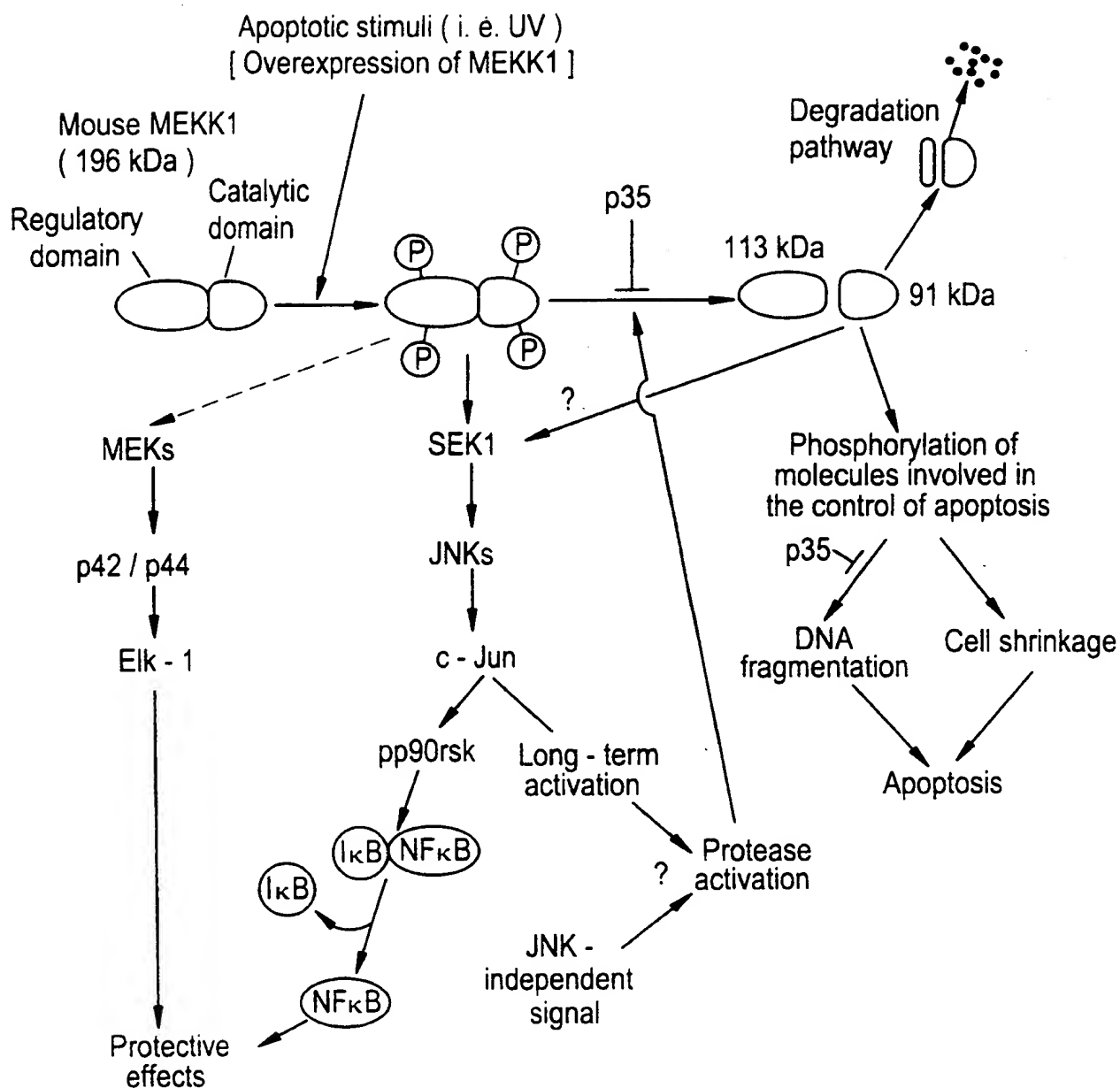


FIG.6



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Lipman-Pearson Protein Alignment

Ktuple: 2; Gap Penalty: 4; Gap Length Penalty: 12

	Similarity Index	Gap Number	Gap Length	Consensus Length
(1>1493)	94.1	4	10	1498
(1>1493)				
NSGGGSGGSL SAGAASGSSQPSISGDVVEACCSVLSIVCADPVYKVVYAALKTLRAMLVY				660
TSGGGSGGSL SAGAASGSSQPSISGDVVEAFCSVLSIVCADPVYKVVYAALKTLRAMLVY				660
TPCHSLAERIKLORLLRPVVDITLVKCADANSRTSQLSISTVLELCKGOAGELAVGREIL				720
TPCHSLAERIKLORLLRPVVDITLVKCADANSRTSQLSISTLLELCKGOAGELAVGREIL				720
KAGSIGVGGVDYVLSCLGNQAESNNWQELLGRCLIDRLLLEFPAEFYPHIVSTOVSQA				780
KAGSIGVGGVDYVLSCLGNQAESNNWQELLGRCLIDRLLLEISAEFYPHIVSTOVSQA				780
EPVEIRYKKLLSLLTFALOSIDNSHSMVGKLSRRILSSARMVTAVPAVFSKLVTLNLS				840
EPVEIRYKKLLSLLAFALOSIDNSHSMVGKLSRRILSSARMVTTVPPLFSKLVTLMSAS				840
GSTHFTMRMRRLMAIADEVEIAEVIQLGVEDTVDGHQDSLOAVAPTSCLENSLEHTVHR				900
GSSHFAARMRRRLMAIADEVEIAEVIQLGSEDTLDGQDSSQALAPPRYPSSSLEHTAHV				900
EKTGKGLSATRLSASSEDISDRLAGYSVGLPSSSTTEQPKPAVQTKGRPHSQCLNSSLPS				960
EKTGKGLKATRLSASSEDISDRLAGYSVGLPSSATTEQPKPTVQTKGRPHSQCLNSSLPS				960
HAQLMFPAAPSAPCSSAPSVP-----DISKHRPQAFVPCKIPASAPQTKRFSLOFQRNCS				1010
PPQLMFPAISAPCSSAPSVPAGSVTDASKHRPRAFVPCKIPASAPQTKRFSLOFQRTCS				1010
EHRDSQQLSPVFTQSRPPSSNIHRPKPSRPVPGSTSKLGDATKSSMTLDLGSASRCDDS				1070
ENRDSEKLSPVFTQSRPPSSNIHRKASRPVPGSTSKLGDASKNSMTLDLNSASQCDDS				1070
FGGGGNSGNAVIPSDETFTVPTVEDKCRLOVNTLNSSIEDLLEASMPSSDITVTFKSEYA				1130
FGSGSNSGSAVIPSEETAFTPAEDKCRLOVNPENLNSSIEDLLEASMPSSDITVTFKSEYA				1130
VLSPEKAENDDTYKDDVNHNOCKEKEAEAEALAIAMAMSASQDALPIVPOQVNGE				1190
VLSPEKAESDDTYKDDVNHNOCKEKEAEAEALAIAMAMSASQDALPIVPOQVNGE				1190

FIGURE 7A

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Lipman-Pearson Protein Alignment

Ktuple: 2; Gap Penalty: 4; Gap Length Penalty: 12

Sequence	Similarity Index	Gap Number	Gap Length	Consensus Length	
(1>1493)	(1>1493)	94.1	4	10	1498
10 20 30 40 50 60 MAAAAGDRASSSGFPGAAAASPEAGGGGGGGGALOGSGAPAAGAAGLLREPGSAGRERAD MAAAAGDRASSSGFPGAAAASPEA---GGGGGALOGSGAPAAGA-GLLRETGSAGRERAD 10 20 30 40 50 70 80 90 100 110 120 WRRQLRKVRSVELDQLPEQLFLAAASPPCPSTSPSPPEPADAAGASRFQPAAGPPPPG : WRRQLRKVRSVELDQLPEQLFLTA-SPPCPSTSPSPPEPADAAGASGFQPAAGPPPPG 60 70 80 90 100 110 130 140 150 160 170 180 AASRCGSHSAELAAARDSGARSPAGAEPPSAAAPSGREMENKETLKGLHKMEDRPEERMI AASRCGSHSAELAAARDSGARSPAGAEPPSAAAPSGREMENKETLKGLHKMDDRPEERMI 120 130 140 150 160 170 190 200 210 220 230 240 REKLKATCMPAWKHEWLERRRRGPVVVKPIPIKGDGSEVNNLAAEPOGEGQAGSAAPAP : REKLKATCMPAWKHEWLERRRRGPVVVKPIPIKGDGSEMSNLAELQEGQAGSAAPAP 180 190 200 210 220 230 250 260 270 280 290 300 KGRSPSPGSSPSGRSVKPESPGYRRKRVSPVPFQSGRITPPRRAPSPDGFSPYSPEETS KGRSPSPGSSPSGRSGKPESPGYRRKRVSPVPFQSGRITPPRRAPSPDGFSPYSPEETS 240 250 260 270 280 290 310 320 330 340 350 360 RRVNKMVRARLYLLQOIGPNSFLIGGSDPNKYRVFIGPONCSCGRGAFCHLLFVMLRV : RRVNKMVRARLYLLQOIGPNSFLIGGSDPNKYRVFIGPONCSCGRGTFCIHLFVMLRV 300 310 320 330 340 350 370 380 390 400 410 420 FQLEPSDPMWLWRKTLKNFEVESLFQKYHSRRSSRIKAPSRNTIOKFVSRMSNSHTLSSSS FQLEPSDPMWLWRKTLKNFEVESLFQKYHSRRSSRIKAPSRNTIOKFVSRMSNCHTLSSSS 360 370 380 390 400 410 430 440 450 460 470 480 TSTSSSENSIKDEEEOMCPICLLGMLDEESLTVCEGDCRNKLHHHCMSIWAECCRNRREP TSTSSSENSIKDEEEOMCPICLLGMLDEESLTVCEGDCRNKLHHHCMSIWAECCRNRREP 420 430 440 450 460 470 490 500 510 520 530 540 LICPLCRSKWRSHDFYSHELSSPVESPAASLRAVQPPSPQPPVAGSQRNRNQEESFNLTHTF : LICPLCRSKWRSHDFYSHELSSPVDSPSLRGVQPPSPQPPVAGSQRNRNQESNFTHTY 480 490 500 510 520 530 550 560 570 580 590 600 GTQOIPSAKYDLAEPWIOVFGMELVGCLFSRNWNVREMLRRLSHOVSGALLANGESTG GTQOIPPAYKDLAEPWIOAFGMELVGCLFSRNWNVREMLRRLSHOVSGALLANGESTG 540 550 560 570 580 590					

FIGURE 7B

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f

Lipman-Pearson Protein Alignment

Ktuple: 2; Gap Penalty: 4; Gap Length Penalty: 12

		Similarity Index	Gap Number	Gap Length	Consensus Length
(1>1493)	(1>1493)	94.1	4	10	1498
↖1200	↖1210	↖1220	↖1230	↖1240	↖1250
DI III I OODTPETLPGHTKAKOPYREDAEWLKGQO IGLGAFSSCYQAQDVGTGLMAYKOV					
DI III I OODTPETLPGHTKANEPYREDTEWLKGQO IGLGAFSSCYQAQDVGTGLMAYKOV					
↖1200	↖1210	↖1220	↖1230	↖1240	↖1250
↖1260	↖1270	↖1280	↖1290	↖1300	↖1310
TYVRNTSSEQEEVVEALREE I RM MGH L NHPNI I RMLGATCEKSNYNLF IEWMAGGSVAHL					
TYVRNTSSEQEEVVEALREE I RM MSH L NHPNI I RMLGATCEKSNYNLF IEWMAGASVAHL					
↖1260	↖1270	↖1280	↖1290	↖1300	↖1310
↖1320	↖1330	↖1340	↖1350	↖1360	↖1370
LSKYGAFKESVVINYTEQLLRGLSYLHENQ I IHRDVKGANLL IDSTGQRLRIADFGAAAR					
LSKYGAFKESVVINYTEQLLRGLSYLHENQ I IHRDVKGANLL IDSTGQRLRIADFGAAAR					
↖1320	↖1330	↖1340	↖1350	↖1360	↖1370
↖1380	↖1390	↖1400	↖1410	↖1420	↖1430
LASKGTGAGEFQGOLLGT I AFMAPEVLRGQOYGRSCDVWSVGCAI IEMACAKPPWNAEKH					
LASKGTGAGEFQGOLLGT I AFMAPEVLRGQOYGRSCDVWSVGCAI IEMACAKPPWNAEKH					
↖1380	↖1390	↖1400	↖1410	↖1420	↖1430
↖1440	↖1450	↖1460	↖1470	↖1480	↖1490
SNHLALIFKIASATTAPSI PSHLSPGLRDVAVRCLELQPD RPPSRELLKHPVFR TTW					
SNHLALIFKIASATTAPSI PSHLSPGLRDVALRCLELQPD RPPSRELLKHPVFR TTW					
↖1440	↖1450	↖1460	↖1470	↖1480	↖1490

FIGURE 7C

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MEKK 1

rat	MAAAAGDRASSSGFPGAAAASPEA---GGGGGALQGSQAPAAG-AGLLRETGSAGRE
mouse	MAAAAGDRASSSGFPGAAAASPEAGGGGGGGGALQGSQAPAAGAAGLLREPGSAGRE
rat	RADWRRQQLRKVRSVELDQLPEQPLFL-TASPPCPSTSPSPPEPADAAGASGFQPA
mouse	RADWRRQQLRKVRSVELDQLPEQPLFLAAASPPCPSTSPSPBPADAAGASRFQPA
rat	GPPPPGAASRCGSHSAELAAARDSGARSPAGAEPPSAAAPSGREMNKETLKGLHKM
mouse	GPPPPGAASRCGSHSAELAAARDSGARSPAGAEPPSAAAPSGREMNKETLKGLHKM
rat	DDRPEERMIREKLKATCMPAWKHEWLERRNRRGPFVVVKPIPIKGDGSEMSNLAAELQ
mouse	EDRPEERMIREKLKATCMPAWKHEWLERRNRRGPFVVVKPIPIKGDGSEVNNLAAEPQ
rat	GEGQAGSAAPAPKGRSPSPGSSPSGRSGKPSGVRKRVSFVFFQSGRITPPRRA
mouse	GEGQAGSAAPAPKGRSPSPGSSPSGRSVKPSGVRKRVSFVFFQSGRITPPRRA
rat	PSPDGFSPYSPEETSRRVNKVMRARLYLLQQIGPNSFLIGGDSFDNKYRVFIGPQNC
mouse	PSPDGFSPYSPEETSRRVNKVMRARLYLLQQIGPNSFLIGGDSFDNKYRVFIGPQNC
rat	SCGRGTFCIHLFVMLRVFQLEPSDFMLWRKTLKNFEVESLFQKYHSRRSSRIKAPS
mouse	SCGRGAFCIHLFVMLRVFQLEPSDFMLWRKTLKNFEVESLFQKYHSRRSSRIKAPS
rat	RNTIQKFVSRMSNCHTLSSSSTSTSSSENSIKDEEQMCPICLLGMLDEESLTVCE
mouse	RNTIQKFVSRMSNCHTLSSSSTSTSSSENSIKDEEQMCPICLLGMLDEESLTVCE
rat	GCRNKLHHHCMSIWAEECRNRNREPLICPLCRSKWRSHDFYSHELSSPVDSPSLRGV
mouse	GCRNKLHHHCMSIWAEECRNRNREPLICPLCRSKWRSHDFYSHELSSPVESPASLRV
human	NKLHHHCMSIWAEECRNRN PLICPLCRS WRSHDFYSHELSSPVDSPSSL
rat	QQPSSPOQPVAGSQRNQNESFNLTHYGTQQIPFAYKDLAEPWIQVFGMELVGCCLFS
mouse	QQPSSPOQPVAGSQRNQNESFNLTHYGTQQIPFAYKDLAEPWIQVFGMELVGCCLFS
human	Q V HPLAGS RRNQNESFNLTHYGTQQIPFAYKDLAEPWIQVFGMELVGCCLFS
rat	RNWNVREMA LRRLSHDVSGALLANGESTGTSGGGSGGSLSAGAASGSSQPSISGDV
mouse	RNWNVREMA LRRLSHDVSGALLANGESTGNSGGSGGSLSAGAASGSSQPSISGDV
human	RNWNVREMA LRRLSHDVSGALLANGESTGNSGGSGGSSPSGGATSG SQTS SGD
rat	VEAFCSVLIVCADPVYKVYVAALKTLRAMLVYTPCHSLAERIKLQRLLRPVVDLIL
mouse	VEACCSVLIVCADPVYKVYVAALKTLRAMLVYTPCHSLAERIKLQRLLRPVVDLIL
human	VEACC
rat	VKCADANSRTSQLSISTVLELCKGQAGELAVGREILKAGSIGVGGVDYVLSLILGNQ
mouse	VKCADANSRTSQLSISTVLELCKGQAGELAVGREILKAGSIGVGGVDYVLSLILGNQ
human	
rat	AESNNWQELLGRLCLIDRLLEISAEFYPHIVSTDVSQAEFVEIRYKLLSLLAFAL
mouse	AESNNWQELLGRLCLIDRLLEFPAEFYPHIVSTDVSQAEFVEIRYKLLSLLTFAL
human	PAEFYPHIVSTDVSQAEFVEIRYKLLSLL FA
rat	QSIDNSHSMVGKLSRRIYLSSARMVTVPPPIFSKLVTMLNAGSSHFARMRRRLMAI
mouse	QSIDNSHSMVGKLSRRIYLSSARMVTVPAVFSKLVTMLNAGSTHFTMRRLMAI
human	K ID SHSMVG SR DISLCYDDGRSAVCPPSW PCLMLLGSTHFTMRRLMAI

FIGURE 8A

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rat	ADEVEIAEVIQLGSEDTLDGQQDSSQALAPPRYPSSSLEHTAHVEKTGKGLKATRL
mouse	ADEVEIAEVIQLGVEDTVDGHQDSLQAVAPTSCLENSLEHTVHREKTGKGLSATRL
human	ADEVEIAEVIQLGEVDTVDGHQDSLRLALAPASCRENSLEHTVHREKTGKGLSATRL
rat	SASSEDISDRLAGVSVGLPSSATTEQPKPTVQTKGRPHSQCLNSSPLSPPQLMFPAT
mouse	SASSEDISDRLAGVSVGLPSSSTTEQPKPAVQTKGRPHSQCLNSSPLSHAQLMFPAP
human	STSSEEISDRLAGVSVGFPSSTTEQPKPAVQTKGRPHSQCLNSSPLSHAQLMFPAP
rat	SAPCSSAPSVPAAGSVTDASKHRPRAFPVCKIPASAPQTKRKFSLQFQRTCSNRDSE
mouse	SAPCSSAPSVP-----DISKHRPQAFVPCIPASAPQTKRKFSLQFQRTCSNRDSD
human	SAPCSSAP VP DISKHRPQAFVPCILPHLPQTKRKFSLQFQRN EHRDQT
rat	KLSPVFTQSRPPSSNIHRAKASRPVPGSTSKLGDASKNSMTLDLNSASQCDDSFSGS
mouse	QLSPVFTQSRPPSSNIHRPKPSRPVPGSTSKLGDATKSSMTLDLGSASRCDDSFQGG
human	QLSPVFTQSQDPTSSNIHRPKPDRPAPGSTSKLGDATKSSMTLDLGCRCDDSFQGG
rat	GSNSGSAVIPSEETAFTPAEDKCRLDVNPENLSSIEDLLEASMPSSDTTVTFKSEVA
mouse	GGNSGSAVIPSDETVFTPVEDKCRLDVNPENLSSIEDLLEASMPSSDTTVTFKSEVA
human	GGNSGSAVIPSDETVFTPVEDKCRLDVNPENLSSIEDLLEASMPSSDTTVTFKSEVA
rat	VLSPEKAESDDTYKDDVNHNNQCKEKEAEAEAEALAMAMSASQDALPIVPQLQVE
mouse	VLSPEKAENDDTYKDDVNHNNQCKEKEAEAEAEALAMAMSASQDALPIVPQLQVE
human	VLSPEKAENDDTYK VY
rat	NGEDIIIIQQDTPETLPGHTKANEPYREDTEWLKGOQIGLGAFFSSCYQAQDVGTGTL
mouse	NGEDIIIIQQDTPETLPGHTKAKQPYREDAEWLKGQOIGLGAFFSSCYQAQDVGTGTL
human	VIQQDTPETLPGHTKAKQPYREDAEWL G QIGLGHF
rat	MAVKQVTYVRNTSSEQEEVVEALREEIRMMSHLNHPNIIIRMLGATCEKSNYNLFIEW
mouse	MAVKQVTYVRNTSSEQEEVVEALREEIRMMGHLNHPNIIIRMLGATCEKSNYNLFIEW
human	EEIR MSHLNHP IIRMLG TGKKNY LFIEW
rat	MAGASVAHLLSKYGAFKESVVINYTEQLLRGLSYLHENQIIHRDVKGANLLIDSTGQ
mouse	MAGGSVAHLLSKYGAFKESVVINYTEQLLRGLSYLHENQIIHRDVKGANLLIDSTGQ
human	MAGGSVAHLLSKYGAF ESVVI YTEQ LRGLSYLHENQIIH DVKGANLLID TG
rat	RLRIADFGAAARLASKGTGAGEFQGLLGTIAFMAPEVLRGQOYGRSCDVWSVGCAI
mouse	RLRIADFGAAARLASKGTGAGEFQGLLGTIAFMAPEVLRGQOYGRSCDVWSVGCAI
human	RLRIADFGAAA LASKG GAGEFQGL GTIAFMAPEV RG QYGRSCDVWSVGCAI
rat	IEMACAKPPWNAEKHSNHLALIFKIASATTAPSIPSHLSPLGRDVALRCLELQPQDR
mouse	IEMACAKPPWNAEKHSNHLALIFKIASATTAPSIPSHLSPLGRDVAVRCLQLQPQDR
human	IEMACAKPPWNAEKHSNHLALIKKIASATTAPSIPSHLSPLGRNVALRCLELQPQDR
rat	PPSRELLKHPVFRTTW
mouse	PPSRELLKHPVFRTTW
human	PPSRELLKHPVFRTT

FIGURE 8B

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